IN THE SPECIFICATION

Please delete the entire Sequence Listing as originally submitted and enter in its place the Substitute Sequence Listing submitted herewith. The Substitute Sequence Listing is submitted in both paper and CRF versions, along with required statement declaring that the paper and CRF versions are identical and do not introduce any new matter.

Please delete the paragraph at page 15, lines 18-27, and insert in its place the following paragraph:

-- Proteolytic tryptases are cleavable and self-assembling tryptases that form into enzymatically-active tetramers. Non-proteolytic tryptases are not cleavable. Cleavage is required for spontaneous assembly. Thus, non-proteolytic tryptases do not self-assemble. As is shown in the amino acid alignment of **Fig. 1** **(see SEQ. ID. NO: 52)**, the proteolytic tryptases of humans share certain sequence similarities. In particular, the amino acids RV are found at amino acids at positions -3 and -2 from amino acid 1, **which is shown as the ▼ symbol in Fig. 1.** ~~which~~ **The ▼ symbol** is the first amino acid of the cleaved proteolytic tryptase**, and corresponds to residue 31 of SEQ. ID. NO: 52**. The RV motif has been implicated in the cleavage of proteolytic tryptase. The RV motif is absent in α-tryptase **(SEQ. ID. NO: 52)**, which is not cleavable, and thus does not self-assemble into tetramers. --

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Please delete the two contiguous paragraphs at page 30, lines 15-29, and insert in their place the following paragraphs:

-- The active sites of tryptase have been predicted to be located at seven loops (A, B, C, D, 3, 1, and 2) as shown in **Fig. 1**. To confirm this, mutations were made to amino acids 44, 91, and 194 **as shown in Fig. 1. These three residues correspond to residues 74, 121, and 224 of SEQ. ID. NO: 52**. Non-conserved changes were made in various amino acids. Amino acids 44, 91, and 194 were changed to alanine. However, amino

acids can be mutated to any non-charged residue. According to molecular modeling, these single point mutations were not expected to disrupt the secondary structure.

As can be seen from **Fig. 1**, amino acid 44 **(residue 74 of SEQ. ID. NO: 52)** is located within the putative B loop, amino acid 91 **(residue 121 of SEQ. ID. NO: 52)** is located in the C terminus direction to loop C, and amino acid 194 **(residue 224 of SEQ. ID. NO: 52)** is within loop 1. Amino acids 44, 91, and 194 are called the catalytic triad. To determine whether the active sites for proteolytic tryptase include histidine at residue 44, asparagine at residue 91, and serine at residue 194, mutants in the putative active sites were generated with the QuikChange™ Site Directed Mutagenesis Kit (Stratagene, LaJolla, California) (described in detail in Example 1c). --